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SEQUENCE LISTING

<110> The Scripps Research Institute
Zhang, Zhiwen
Alfonta, Lital
Schultz, Peter

<120> SELECTIVE INCORPORATION OF 5-HYROXYTRYPTOPHAN INTO PROTEINS IN
MAMMALIAN CELLS

<130> 54A-001020PC

<160> 7

<170> PatentIn version 3.2

<210> 1

<211> 993

<212> DNA

<213> Artificial

<220>

<223> encodes Val144Pro mutant of Bacillus subtilis tryptophanyl-tRNA
synthetase

<400> 1

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gcagtaacgg attctgaagg cattgtcaaa ttgataagg aaaacaaacc gggcggtttcc	720
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<210> 2

<211> 330

<212> PRT

<213> Artificial

<220>

<223> Val144Pro mutant of Bacillus subtilis tryptophanyl-tRNA

synthetase

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Met Lys Gln Thr Ile Phe Ser Gly Ile Gln Pro Ser Gly Ser Val Thr
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 35 40 45
 Pro Gln Asp Arg Leu Glu Leu Arg Lys Asn Ile Arg Asn Leu Ala Ala
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 Leu Tyr Leu Ala Val Gly Leu Asp Pro Glu Lys Ala Thr Leu Phe Ile
 65 70 75 80
 Gln Ser Glu Val Pro Ala His Ala Gln Ala Gly Trp Met Met Gln Cys
 85 90 95
 Val Ala Tyr Ile Gly Glu Leu Glu Arg Met Thr Gln Phe Lys Asp Lys
 100 105 110
 Ser Lys Gly Asn Glu Ala Val Val Ser Gly Leu Leu Thr Tyr Pro Pro
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 130 135 140
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 165 170 175
 Ile Pro Lys Val Gly Ala Arg Ile Met Ser Leu Asn Asp Pro Leu Lys
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 Lys Met Ser Lys Ser Asp Pro Asn Gln Lys Ala Tyr Ile Thr Leu Leu
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 Asp Glu Pro Lys Gln Leu Glu Lys Lys Ile Lys Ser Ala Val Thr Asp
 210 215 220
 Ser Glu Gly Ile Val Lys Phe Asp Lys Glu Asn Lys Pro Gly Val Ser
 225 230 235 240
 Asn Leu Leu Thr Ile Tyr Ser Ile Leu Gly Asn Thr Thr Ile Glu Glu
 245 250 255

Leu Glu Ala Lys Tyr Glu Gly Lys Gly Tyr Gly Glu Phe Lys Gly Asp
 260 265 270

Leu Ala Glu Val Val Val Asn Ala Leu Lys Pro Ile Gln Asp Arg Tyr
 275 280 285

Tyr Glu Leu Ile Glu Ser Glu Glu Leu Asp Arg Ile Leu Asp Glu Gly
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Asn Ala Met Gly Leu Gly Arg Lys Arg Arg
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<210> 3
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 <212> RNA
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 <223> mutant opal supressor tRNA

<400> 3
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 uaccgccccu g 71

<210> 4
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 <212> RNA
 <213> Bacillus subtilis

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 uacugccccu gcc 74

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<223> oligonucleotide probe

<400> 7

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23

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atcggtgcaa tgaagcagtt tgtcgaactg cagcatgatt ataacagcta tttttgcatc 120
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aatctcgcgg cgctttactt agctgtcggc cttgatccag aaaaagcaac attgtttatt 240
cagtcagagg tccccgcaca tgcgcaggcc ggatggatga tgcagtgtgt cgcctatata 300
ggcgagcttg agcggatgac tcaatttaag gacaaatcca aaggcaatga agctgtcgtc 360
tccggcctgt taacatatcc gccgctgatg gccgctgata ttctgctgta cggaacggat 420
cttgatcctc ccggcgagga tcaaaagcag caccttgagc tgacgcggaa tcttgagaa 480
cgcttcaaca aaaaatacaa cgacatcttt acgattccgg aagtgaataa tccaaaagtc 540
ggtgcacgta tcatgtctct gaatgatccg ctgaagaaaa tgagcaaata tgatccgaat 600
cagaaagctt atattacatt gctggatgag ccgaagcagc ttgaaaagaa aatcaaaagc 660
gcagtaacgg attctgaagg cattgtcaaa ttgataagg aaaacaaacc gggcgtttcc 720
aaccttctta caatttatcc aatcctcggc aatacgacaa ttgaagagct tgaagcaaag 780
tacgaaggaa aaggctacgg cgagtttaaa ggtgatttgg cagaagtcgt agtgaacgca 840
ttaaaaccga tccaggaccg ctattacgag ctgatagaat ctgaagaatt agaccggatt 900
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<211> 330
<212> PRT
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Met Lys Gln Thr Ile Phe Ser Gly Ile Gln Pro Ser Gly Ser Val Thr
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Leu Gly Asn Tyr Ile Gly Ala Met Lys Gln Phe Val Glu Leu Gln His
20 25 30

Asp Tyr Asn Ser Tyr Phe Cys Ile Val Asp Gln His Ala Ile Thr Val
35 40 45

Pro Gln Asp Arg Leu Glu Leu Arg Lys Asn Ile Arg Asn Leu Ala Ala
50 55 60

Leu Tyr Leu Ala Val Gly Leu Asp Pro Glu Lys Ala Thr Leu Phe Ile
65 70 75 80

Gln Ser Glu Val Pro Ala His Ala Gln Ala Gly Trp Met Met Gln Cys
85 90 95

Val Ala Tyr Ile Gly Glu Leu Glu Arg Met Thr Gln Phe Lys Asp Lys
100 105 110

Ser Lys Gly Asn Glu Ala Val Val Ser Gly Leu Leu Thr Tyr Pro Pro
115 120 125

Leu Met Ala Ala Asp Ile Leu Leu Tyr Gly Thr Asp Leu Val Pro Pro
130 135 140

Gly Glu Asp Gln Lys Gln His Leu Glu Leu Thr Arg Asn Leu Ala Glu
145 150 155 160

Arg Phe Asn Lys Lys Tyr Asn Asp Ile Phe Thr Ile Pro Glu Val Lys
165 170 175

Ile Pro Lys Val Gly Ala Arg Ile Met Ser Leu Asn Asp Pro Leu Lys
180 185 190

Lys Met Ser Lys Ser Asp Pro Asn Gln Lys Ala Tyr Ile Thr Leu Leu
195 200 205

Asp Glu Pro Lys Gln Leu Glu Lys Lys Ile Lys Ser Ala Val Thr Asp
210 215 220

Ser Glu Gly Ile Val Lys Phe Asp Lys Glu Asn Lys Pro Gly Val Ser
225 230 235 240

Asn Leu Leu Thr Ile Tyr Ser Ile Leu Gly Asn Thr Thr Ile Glu Glu
245 250 255

Leu Glu Ala Lys Tyr Glu Gly Lys Gly Tyr Gly Glu Phe Lys Gly Asp
260 265 270

Leu Ala Glu Val Val Val Asn Ala Leu Lys Pro Ile Gln Asp Arg Tyr
 275 280 285

Tyr Glu Leu Ile Glu Ser Glu Glu Leu Asp Arg Ile Leu Asp Glu Gly
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Ala Glu Arg Ala Asn Arg Thr Ala Asn Lys Met Leu Lys Lys Met Glu
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Asn Ala Met Gly Leu Gly Arg Lys Arg Arg
 325 330

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 aggggcgugg cuuacgguu gagcagaggu cucaaaacc uccggugugg guucgauucc 60
 uaccgccccu g 71

<210> 4
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 <212> RNA
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<400> 4
 aggggcgauag uuuaacgguu gaacagaggu cucaaaacc uccggugugg guucgauucc 60
 uacugccccu gcca 74

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